



1 GAATTTGGCC CTCGAGGCCA AGAATTCGCG ACAGGGCGCG GCGCCACGCG CAGGCAGAGC GCTGTGCGCAT CCCGGGCGTC CACCCGCCAT GGGGCTCTCC
CTTAAACCGG GAGCTCCGGT TCTTAAGCCG TGCTCCGCGC CGCGGGTCGC GTCCGTCTCG CGACAGCGTA GGGCCCGCAG Me tGlyLeuSer
1
201 TGGAGCCCCG GACCTCCACT GCTGATGATC CTGCTACTGG TGCTGTCTGT GTGGTGCCCA CTGGAGGAGC GAAACTCCCT TGCCACAGAG AACAGGTTTG
ACCTCGGGCG CTGGAGGTGA CGACTACTAG GACGATGACC ACACAGCAA CACCGACGGT GAACCTCGTC CTTTGAGGGA ACGGTGTCTC TTGTCCAAAC
5 TrpSerProA rgProProLe uLeuMetile uLeuLeuV alleuSerle uTrpLeuPro LeuGlyAlag lyAsnSerle uAlaThrGlu AsnArgPheVal
201 TGAACAGCTG TACCCAGGCC AGAAAGAAAT GCGAGGCTAA TCCCGCTTGC AAGGCTGCCT ACCAGCACCT GGGCTCCTGC ACCTCCAGTT TAAGCAGGCC
ACTTGTGAC ATGGGTCCGG TCTTTCTTTA CGCTCCGATT AGGCGAAGC TTCCGACGGA TGGTCTGTGA CCCGAGGAGC TGGAGGTCAA ATTCTGTCGG
39 AsnSerCy sThrGlnAla ArgLysLysC ysGluAlaAs nProAlaCys LysAlaAlaT yrGlnHisLe uGlySerCys ThrSerSerL euSerArgPro
301 GCTGCCCTTA GAGGAGTCTG CCATGCTCTG AGACTGCCTA GAGGCAGCAG AACAACTCAG GAACAGCTCT CTGATAGACT GCAGGTGCCA TCGGCGCATG
CGACGGGAAT CTCCTCAGAC GGTACAGACG TCTGACGGAT CTCGTCGTC TTGTTGAGTC CTTGTGCGAG GACTATCTGA CGTCCACGGT AGCCGCGTAC
72 LeuProLeu GluGluSera laMetSerAl aAspCysLeu GluAlaAlaG luGlnLeuAr gAsnSerSer LeuIleAspC ysArgCysHi sArgArgMet
401 AAGCACCAAG CTACCTGTCT GGACATTTAT TGGACCGTTC ACCCTGCCCG AAGCCTTGGT GACTACGAGT TGGATGTCTC ACCCTATGAA GACACAGTGA
TTCTGTGTTT GATGACAGA CCTGTAAATA ACCTGGCAAG TGGGACGGC TTCCGAACCA CTGATGCTCA ACCTACAGAG TGGGATACTT CTGTGTCACT
105 LysHisGlnA laThrCysLe uAspIleItyr TrpThrValH isProAlaAr gSerLeuGly AspTyrGluL euAspValse rProTyrGlu AspThrValThr
501 CCAGCAAAAC CTGGAAAATG AATCTTAGCA AGTTGAACAT GCTCAAACCA GACTCGGACC TCTGCCTCAA ATTTGCTATG CTGTGTACTC TTCACGACAA
GGTCTGTTTG GACCTTTTAC TTAGAATCTG TCAACTTGTA CGAGTTTGGT CTGACCTGG AGACGGAGTT TAAACGATAC GACACATGAG AAGTGTCTGT
139 SerLysPr oTrpLysMet AsnLeuSerL ysLeuAsnMe tLeuLysPro AspSerAspL euCysLeuLy sPheAlaMet LeuCysThrL euHisAspLys
601 GTGTGACCGC CTGCGCAAGG CCTACGGGGA GGCATGCTCA GGGATCCGCT GCCAGGCGCA CCTCTGCCTA GCCCAGCTGC GCTCCTTCTT TGAGAAGGCA
CACACTGGCG GACGCGTTC GGATGCCCT CGTACGAGT CCTAGGCGA CGGTCCGGT GGAGACGGAT CGGTTCGACG CGAGGAAGAA ACTCTTCCGT
172 CysAspArg LeuArgLysA laTyrGlyG l uAlaCysSer GlyIleArgC ysGlnArgHi sLeuCysLeu AlaGlnLeuA rgSerPhePh eGluLysAla
701 GCAGAGTCCC ACGCTCAGGG TCTGCTGCTG TGTCCCTGTG CACCAAGAAGA TGCGGGCTGT GGGGAGCGGC GCGTAACAC CATCGCCCC AGTTGCGCCC
CGTCTCAGG TGCGAGTCCC AGACGACGAC ACAGGGACAC GTGGTCTTCT ACGCCGACAC CCCCTCGCCG CCGCATTTGT GTAGCGGGG TCAACGCGGG
205 AlaGluSerH isAlaGlnG l yLeuLeuLeu CysProCysA laProGluAs palaGlyCys GlyGluArga rgArgAsnTh rIleAlaPro SerCysAlaLeu
801 TGCCTTCTGT AACCCCAAT TGCCTGGATC TGCCTGGCTT TGCGGAGCTT GACCTTTGT GCAGATCAGC CCTGATGGAC TTCCAGACCC ACTGTCTATCC
ACGGAAGACA TTGGGGGTTA ACGGACCTAG ACGCTCGAA GACGCGACGC CTGGGAACA CGTCTAGTGC GGACTACCTG AAGGTCTGGG TGACAGTAGG
239 ProSerVa lThrProAsn CysLeuAspL euArgSerPh eArgSerAla AspProLeuC ysArgSerAr gleuMetAsp PheGlnThrH isCysHisPro
901 TATGGACATC CTTGGGACTT GTGCAACTGA GCAGTCCAGA TGCTGCGGG CATACCTGGG GCTGATTGG ACTGCCATGA CCCAAACTT CATCAGCAAG
ATACCTGTAG GAACCTGAA CACGTTGACT CGTCAGGTCT ACAGACGCC GTATGGACCC CGACTAACCC TGACGGTACT GGGGTTTGA GTAGTCGTTT
272 MetAspIle LeuGlyThrC ysAlaThrG l uGlnSerArg CysLeuArga laTyrLeuG l yLeuIleGly ThrAlaMetT hrProAsnPh eIleSerLys

FIG. 1A

1001 GTCAACACTA CTGTTGCCCTT AAGCTGCACC TGCCGAGGCA GCGCAACCT ACAGGACGAG TGTGAACAGC TGAAGAAGTC CTTCTCCCAG AACCCCTGCC
CAGTTGTGAT GACAACGGAA TTCCAGCTGG ACGGCTCCGT CGCCGTTGGA TGTCTGCTC ACATTGTCTG ACCTTTCCAG GAAGAGGTC TTGGGGACGG
305 ValAsnThrT hrValAlaLe uSerCysThr CysArgGlys erGlyAsnLe uGlnAspGlu CysGluGlnL euGluArgSe rPheSerGln AsnProCysLeu
1101 TCGTGGAGGC CATTGCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACAGCAA
AGCACCTCCG GTAACGTCGA TTCTACGCAA AGGTGCTGTG CGAGAAGAGG GTCTGACCC GTCTGAGATG AAAAAGTCAC CACGTCGTCG TCTTGTCTGT
339 ValGluAl aileAlaAla LysMetArgp heHisArgGl nLeuPheSer GlnAspTrpA laAspSerTh rPheSerVal ValGlnGlnG InAsnSerAsn
1201 CCCTGCTCTG AGACTGCAGC CCAGGCTACC CATTCTTTCT TTCTCCATCC TTCTCTGAT TCTGTGCAG ACCCTCTGGT AGCTGGGCTT CCTCAGGGTC
GGGACGAGAC TCTGACGTCG GGTCCGATGG GTAAGAAAGA AAGAGGTAGG AAGGAACTA AGACGAGTC TGGGAGACCA TCGACCCGAA GGAGTCCCAG
372 ProAlaLeu ArgLeuGlnP roArgLeuPr oileLeuSer PheSerIleL euProLeuIl eLeuLeuGln ThrLeuTrp
1301 CTTTGTCTC TCCACCACAC CCAGACTGAT TTGCAGCCTG TGGTGGGAGA GAACTCGCCA GCCTGTGGAA CGTGTACAC AGCAACCCCG
GAAACAGGAG AGGTGGTGTG GGTCTGACTA AACGTCGGAC ACCACCTCT CTTGAGCGGT CGGACACCTT CTTCTGCGTC GCACGATGTG TCGTTGGGCC
1401 AACCAACCAG GCATTCCGCA GCACATCCCG TCTGCTCCAG AAGAGGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGCTAG TTTTCAAACC
TTGGTTGGTC CGTAAGCGT CGTGTAGGC AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AAGGCTAGGA CTCGCCGATC AAAAGTTTGG
1501 TCCCTTGCC CTGCTTCCTT CTGGCTCAGG CTGCTCCTCC TTAGGACTTT GTGGTCCAG TTTTGCCTTC TGTCTGTATG GTGATTAGCG GCTCACCTCC
AGGGAACGGG GACGAAGGAA GACCGAGTCC GACGAGGAGG AATCCTGAAA CACCAGGTC AAAACGGAG ACAAGACTAC CACTAATCGC CGAGTGGAGG
1601 AGCGCTTCTT CCTGTTTCCC AGGACCACCC AGAGGCTAAG GAATCAGTCA TTCCCTGTTG CCTTCTCCAG GAAGGCAGGC TAAGGTTCT GAGGTGACTG
TCGCGAAGAA GGACAAAGG TCCTGGTGGG TCTCCGATT CTTAGTCAGT AAGGACAAC GGAAGAGGTC CTTCCGTCCG ATTCCCAAGA CTCCACTGAC
1701 AGAAAAATGT TTCTTTTGTG TGAAGGCTG GTGCTCCAGC CTCCACGTCC CTCTGAATGG AAGATAAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC
TCITTTTACA AAGGAAACAC ACCTTCCGAC CACGAGGTG CACGAGGTG GAGACTTACC TTCTATTTTT GGACGACCAC AGAAGTACG AGACGTTCCG
1801 AATCCTGAAC ATTTGGGCAT GAAGAGCTAA AGTCTTTGG TCTTGTTTAA CTCCTATTAC TGTCCCCAAA TTCCCCTAGT CCCTTGGGTC ATGATTAAAC
TTAGGACTTG TAAACCCGTA CTTCTCGATT TCAGAAACCC AGAACAAATT GAGGATAATG ACAGGGTTTT AAGGGGATCA GGGAACCCAG TACTAATTTG
1901 ATTTTGACTT AAAAAAAA AAAA AAAA
TAAACTGAA TTTTTTTTTT TTTTTT

FIG. 1B

FIG. 2

FIG. 2

hGFra3	1	M	V	R	P	L	N	P	R	P	L	P	P	V	V	L	M	L	L	L	L	L	P	P	S	P	L	P	L	A	G	D	P	L	P	T	E	S	R	L	M	N	S	C	L	Q	A	R	R	K	
mGFra3	1	.	.	M	G	L	S	W	S	P	R	P	P	L	L	M	I	L	L	L	V	L	S	L	W	.	L	P	L	G	A	G	N	S	L	A	T	E	N	R	F	V	N	S	C	T	Q	A	R	K	K
hGFra3	51	C	Q	A	D	P	T	C	S	A	A	Y	H	L	D	S	C	T	S	S	I	S	T	P	L	P	S	E	E	P	S	V	P	A	D	C	L	E	A	A	Q	L	R	N	S	S	L	I	G		
mGFra3	48	C	E	A	N	P	A	C	K	A	A	Y	Q	H	L	G	S	C	T	S	S	L	S	R	P	L	P	L	E	E	S	A	M	S	A	D	C	L	E	A	A	E	Q	L	R	N	S	S	L	I	D
hGFra3	101	C	M	C	H	R	R	M	K	N	Q	V	A	C	L	D	I	Y	W	T	V	H	R	A	R	S	L	G	N	Y	E	L	D	V	S	P	Y	E	D	T	V	T	S	K	P	W	K	M	N	L	S
mGFra3	98	C	R	C	H	R	R	M	K	H	Q	A	T	C	L	D	I	Y	W	T	V	H	P	A	R	S	L	G	D	Y	E	L	D	V	S	P	Y	E	D	T	V	T	S	K	P	W	K	M	N	L	S
hGFra3	151	K	L	N	M	L	K	P	D	S	D	L	C	L	K	F	A	M	L	C	T	L	N	D	K	C	D	R	L	R	K	A	Y	G	E	A	C	S	G	P	H	C	Q	R	H	V	C	L	R	Q	L
mGFra3	148	K	L	N	M	L	K	P	D	S	D	L	C	L	K	F	A	M	L	C	T	L	H	D	K	C	D	R	L	R	K	A	Y	G	E	A	C	S	G	I	R	C	Q	R	H	L	C	L	A	Q	L
hGFra3	201	L	T	F	F	E	K	A	A	E	P	H	A	Q	G	L	L	L	C	P	C	A	P	N	D	R	G	C	G	E	R	R	R	N	T	I	A	P	N	C	A	L	P	P	V	A	P	N	C	L	E
mGFra3	198	R	S	F	F	E	K	A	A	E	S	H	A	Q	G	L	L	L	C	P	C	A	P	E	D	A	G	C	G	E	R	R	R	N	T	I	A	P	S	C	A	L	P	S	V	T	P	N	C	L	D
hGFra3	251	L	R	L	C	F	S	D	P	L	C	R	S	R	L	V	D	F	Q	T	H	C	H	P	M	D	I	L	G	T	C	A	T	E	Q	S	R	C	L	R	A	Y	L	G	L	I	G	T	A	M	
mGFra3	248	L	R	S	F	C	R	A	D	P	L	C	R	S	R	L	M	D	F	Q	T	H	C	H	P	M	D	I	L	G	T	C	A	T	E	Q	S	R	C	L	R	A	Y	L	G	L	I	G	T	A	M
hGFra3	301	T	P	N	F	V	S	N	V	N	T	S	V	A	L	S	C	T	C	R	G	S	G	N	L	Q	E	E	C	E	M	L	E	G	F	F	S	H	N	P	C	L	T	E	A	I	A	A	K	M	R
mGFra3	298	T	P	N	F	I	S	K	V	N	T	T	V	A	L	S	C	T	C	R	G	S	G	N	L	Q	E	C	E	Q	L	E	R	S	F	S	Q	N	P	C	L	V	E	A	I	A	A	K	M	R	
hGFra3	351	F	H	S	Q	L	F	S	Q	D	W	P	H	P	T	F	A	V	M	A	H	Q	N	E	N	P	A	V	R	P	Q	P	W	V	P	S	L	F	S	C	T	L	P	L	I	L	L	S	L	W	
mGFra3	348	F	H	R	Q	L	F	S	Q	D	W	A	D	S	T	F	S	V	V	Q	Q	N	S	N	P	A	L	R	L	Q	P	R	L	P	I	L	S	F	S	I	L	P	L	I	L	L	Q	T	L	W	

FIG. 3

48613 1 MVRPLNPRPLPPVVLMLLLPLPPSPLPLAAGDPLPTESRLMNSCLQARRK
48614 1 MVRPLNPRPLPPVVLMLLLPLPPSPLPLAAGDPLPTESRLMNSCLQARRK

48613 51 CQADPTCSAAHYHLDSTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48614 51 CQADPTCSAAHYHLDSTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG

48613 101 CMCHRRMKNQVACLDIYWTVHRARSLGNYELDVSPYEDTSTKPKWMNLS
48614 101 CMCHRRMKNQVACLDIYWTVHRARSL.....

48613 151 KLNMLKPDSDLCLKFAMLCCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL
48614 127DSDLCLKFAMLCCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL

48613 201 LTFEKA AEPAQGLLLCPCAPNDRGCGERRNTIAPNCALPPVAPNCLE
48614 170 LTFEKA AEPAQGLLLCPCAPNDRGCGERRNTIAPNCALPPVAPNCLE

48613 251 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM
48614 220 LRRLCFSDPLCRSRLVDFQTHCHPMDILGTCATEQSRCLRAYLGLIGTAM

48613 301 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFFSHNPCLTEAIAAKMR
48614 270 TPNFVSNVNTSVALSCTCRGSGNLQEECEMLEGFFFSHNPCLTEAIAAKMR

48613 351 FHSQLFSQDWPHPHTFAVMAHQENPAVRPQPWPVPSLFSC TLPLILLSLW
48614 320 FHSQLFSQDWPHPHTFAVMAHQENPAVRPQPWPVPSLFSC TLPLILLSLW

FIG. 4

DNA48613.orf 1 A T G G T G C G C C C C C T G A C C C G C G A C C G C T G C C G C C C G T A G T C T G A T G T T
GINFRa1.orf 1 A T G A T C T T G G C A A C G T C T T C T G C T C T C T T C T T C T
GINFRa2.orf 1 A T G A T C T T G G C A A C G T C T T C T G C T C T C T T C T T C T

DNA48613.orf 51 G C T G C T G C T G C T G C C G C T G C C G C T G C C T C T G C A G C C G A G A C C C C C
GINFRa1.orf 6 C C T G G C G A C C C T G T A C T T C G C G C T G C C G C T C T T G G A C T T G C T C C T G T C G G
GINFRa2.orf 39 A G A C G A G A C C C T C G C T C T T T G G C A G C C C T T C T C C C T G C A G G C C C C G

DNA48613.orf 101 T T C C A C A G A A G C C G A C T C A T G A A C A G C T G T C T C C A G G C C A G G A G A G
GINFRa1.orf 56 C C G A A G T G A G C G G C G G A G A C C G C C T G G A T T G C G T G A A A G C C A G T G A T C A G
GINFRa2.orf 89 A G C T C A C A C G G C T G G C G C C C C A G T G G A C T G T C C G G G C C A A T G A G C T G

DNA48613.orf 151 T G C C A G G C T G A T C C C A C C T G C A G T G C T G C T A C C A C A C A G C T G G A T T C C T G
GINFRa1.orf 106 T G C C T G A A G A G C A G A C T G C A G C A C A G T A C C G C A C G C T A A G G C A G T G
GINFRa2.orf 139 T G T G C C G C C A T C C A A C T G C A G C T C C G C T A C C G C A C T C T G C G G C A G T G

DNA48613.orf 201 C A C C T C T A G C A T A A G C A C C C A C T G C C C T . . . C A G A G A G C C T T C G G T C C
GINFRa1.orf 156 C G T G G C G G C A A G A G A C C A A C T T C A G C C T G G C A T C C G G C C T G G A G G C C A
GINFRa2.orf 189 C T G G C A G G C G C G A C C G C A C A C C A T G C T G G C C A

DNA48613.orf 248 C T G C T G A C T G C C T G G A G G C A G C A G C A C T C A G G A C A G C T C T G A T A
GINFRa1.orf 206 A G A T G A G T G C C G C A G C G C C A T G G A G G C C C T G A A G C A G A A G T C G C T C T A C
GINFRa2.orf 224 A C A G A G A G T G C C A G G C G C C T T G G A G G T C T T G C A G G A G A G C C G C T G T A C

DNA48613.orf 298 G G C T G C A T G T G C C A C C G G C G C A T G A A G A A C A G G T T G C C T G C T T G G A C A T
GINFRa1.orf 256 A C T G C C G C T G C A A G C G G G G T A T G A A G A A G G A G A A G A C T G C C T G C G C A T
GINFRa2.orf 274 G A C T G C C G C T G C A A G C G G G G C A T G A A G A A G G A G C T G C A G T C T G C A G A T

DNA48613.orf 348 C T A T T G G A C C G T T C A C C G T G C C G C A G C C T T G G T A A C T A T G A G C T G G A T G
GINFRa1.orf 306 T T A C T G G A G C A T G T A C C A G A C C C T G C A G G G A A A T G A T C T G C T G G A G G A T T
GINFRa2.orf 324 C T A C T G G A G C A T C C A C C T G G G G C T G A C C G A G G T G A G G A G T T C T A C G A A G

FIG. 5A

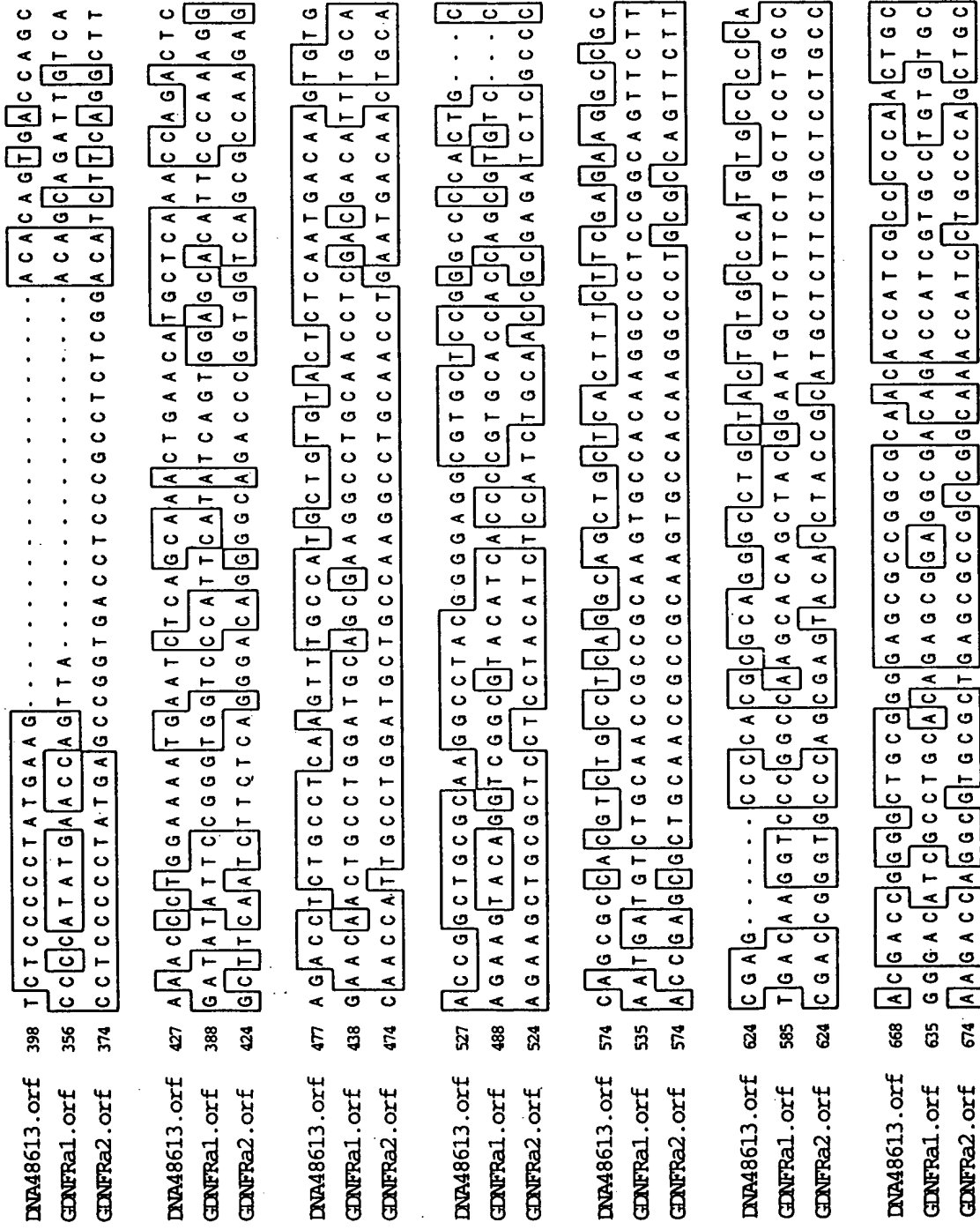


FIG. 5B

DNA48613.orf 718 GCGCTGCC...GCCTGTGGCCCCCAACTGCCCTGGAGCTGGCGGCGCCCTCTG
GENFRa1.orf 685 TCCATATGAAGAGAGGGAAGGCCCAACTGTTGAATTJTGCACTTCTG
GENFRa2.orf 724 TCCATATGAAGAGAGGGAAGGCCCAACTGCCCTGGAGCTGGCGTGGCGTGTG

DNA48613.orf 765 CTCTCTCCGACCCGCTTTGCAGATCAAGCCCTGGTGGATTTCCAGACCCACT
GENFRa1.orf 735 CAAAGACGAATTACATCTGCAGATCTCGCCTTGGCGGATTTTACCAACT
GENFRa2.orf 774 CCGGACTGACCACTGTGTCGTCGCTGGCCGACTTCCATGCCAATT

DNA48613.orf 815 GCCATCCCATGGACATCCTAGAACCTTGTGCAACAGAGCAATCAGA...
GENFRa1.orf 785 GCCAGCCAGAGTCAAGGTCGTGTCAAGCAGCTGTCTAAAGGAATACTACGCT
GENFRa2.orf 824 GTCGAGCCTCCTACCAAGACGGTCAACAGCTGCCCTGCGGACAATTACCAAG

DNA48613.orf 862 ...TGCTCTACGAGCATACCTGGGGCTGATTGGGACTGCCATGACCCCAA
GENFRa1.orf 835 GACTGCTCTCGGCTTCTCGGCTTCTCGGGCTTATTGGCACAAGTCAAGACCCCAA
GENFRa2.orf 874 GCGTGTCTGGGCTCTTATGCTGGCATGATTGGGTTTGAATGACACCTTAA

DNA48613.orf 909 CTGTGTCAAGCAATGTCA...ACACAGTGTGGCCTTAAAGCTGCACT
GENFRa1.orf 885 CTACATAGACTCCAGTA...GCCTCAGTGTGGCCCATGGTGTGACT
GENFRa2.orf 924 CTATGTGGACTCCAGCCCACTGGCATCGTGTGTCCCCCTGGTGCAGCT

DNA48613.orf 953 GCCGAGGCAGTGGCAACCTGCAGGAGGAGTGTGAATGCTGGAAGGGTTC
GENFRa1.orf 929 GCAACAACAGTGGGAACGACCTAGAAAGAGTGTGAAATCTTGAATTTC
GENFRa2.orf 974 GTCGTGGCAGCGGGAACAATGGAGGAGGAGTGTGAAGTTCTCAGGGAAC

DNA48613.orf 1003 TCTCCCAACAACCCCTGCGCTCAACGAGGCCATTGCAGCTAAGATGCGTTT
GENFRa1.orf 979 TTCAAGGACAATACATGTCTTAAATAATGCAATTCAAGCCTTTGGCAATGG
GENFRa2.orf 1024 TTCAACCGAGAACCCCATGCCTCCGGAACGCCATCAGGCCCTTTGGCAACGG

FIG. 5C

DNA48613.orf 1053 T C A C A G C C A A C T C T T C T C C C A G G A C T G G C C A C A C C C T A C C T T T G C T G T G A
 GENFRa1.orf 1029 C T C C G A T G T G A C C G T G T G G C A G C C A G C T T C C C A G T A C A G A C C A C C A C T G
 GENFRa2.orf 1074 C A C G G A C G T G A A C G T G T C C C C A A A G G C C C C T C G T T C A G G C C A C C C A G G

 DNA48613.orf 1103 T G G C A C A C A C A G A A T G A A A C C C T G C T G T G A G G C C A C A G C C T G G G T G C C C
 GENFRa1.orf 1079 C C A C T A C C A C C A C T G C C C T C G G G T T A G A A C A A A C C C T G G G C C A G C A
 GENFRa2.orf 1124 C C C C T C G G G T G G A G A A G A C G C C T T C T T T G C C A G A T G A C C T C A G T G A C A G T

 DNA48613.orf 1153 T C T C T T T C T C C T G C A C G C T T C C C T T G A T T C T G C T C C T G A G C C T A T G G T A
 GENFRa1.orf 1129 G G G T C T G A G A A T G A A A T T C C C A C T C A T G T T T T G C C A C C G T G T G C A A A T T T
 GENFRa2.orf 1174 A C A G C T T G G G A C C A G T G T C A T C A C C A C C T G C A C G T C T G T C C A G G A G C A

 DNA48613.orf 1203 G
 GENFRa1.orf 1179 A C A G G C A C A G A A G C T G A A A T C C A A T G T C G G G C A A T A C A C A C C T C T G T A
 GENFRa2.orf 1224 G G G C T G A A G G C C A A C A A C T C C A A A G A G T A A G C A T G T G C T T C A C A G A G C

 GENFRa1.orf 1229 T T T C A A T G G T A A T T A T G A A A A G A A G G T C T C G T G C T T C C A G C C A C A T A
 GENFRa2.orf 1274 T C A C G A C A A A T A T C A T C C C A G G G A G T A A C A A G G T G A T C A A A C C T A A C T C A

 GENFRa1.orf 1279 A C C A C A A A T C A A T G G C T G C T C C A A G C T G T G G T C T G A G C C C A C T G C T
 GENFRa2.orf 1324 G G C C C C A G C A G A G C C A G A C C G T C G G C T G C C T T G A C C G T G C T G T C T C T

 GENFRa1.orf 1329 G G T C C T G T G G T A A C C G C T C T G T C C A C C C T A T T A T C T T T A C A G A A A C A T
 GENFRa2.orf 1374 G A T G C T G A A C A G C C T T G T A G

 GENFRa1.orf 1379 C A T A G

FIG. 5D

DNA48613 1 MVRPLNPRPLPPVVLMLLLLLPSPPLPLAAGDPLPTESRLMNSCLQARRK
 GDNFRa1 1 MFLAT--LYFALL-PLLDLLLSA--EVSGGD--R'L--DCVKASDQ
 GDNFRa2 1 MILANVFCLFFFLDETLLRSLASPS--SLQGPELHGWRPPV--DCVRANEL

DNA48613 51 CQADPTCSAAYHHLDSCTSSISTPLP-SEEPSVPADCLEAAQQLRNSSLI
 GDNFRa1 36 CLKEQSCSTKYRTL RQCVAGKETNFSLASGLEAKDECRSAMEALKKKSLEY
 GDNFRa2 47 CAAESNCSSRYRTL RQCLAGRDRN-----TMLANKKECOAAL EVLQESPLY

DNA48613 100 GCMCHRRMKNQVACLDIYWTVHRRARSLGNYELDVSPYEDT VTSKPWKMNLI
 GDNFRa1 86 NCRCKRGMKKEKNCLRIYWSMYQSL-QGNDLLEDSPYEPVNSRLSDIFRV
 GDNFRa2 92 DCRCKRGMKKEQLQCLQIYWSIHLGLTEGEFYEASPYEPVTSRLSDIFRL

DNA48613 150 SKL-----NMLKPPDSDLCLKFAMLC TLNDKCKDRRLRKAYGEAC S-----
 GDNFRa1 135 VPFIS--VEHI--PKGNCLDAAKACNLDDICKKYRSAYITPCTTSVS-
 GDNFRa2 142 ASIFS GTGADPVVSAKSNHCLDAAKACNLNDNCKKLRS SYISICNREIS P

DNA48613 188 GPHCQRHVCLRQLLTFFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAP
 GDNFRa1 179 NDVCNRRKCHKALRQFFDQVPAKHSHYGM LFCSC--RDIAC TERRRQTIVP
 GDNFRa2 192 TERCNRRKCHKALRQFFDRVPSEYTYRMLFCSC--QDQACAERRRQTILP

DNA48613 238 NCALPPVA-PNCLELRRLCFSDPLCRSRLVDFQTHCHP-MDILGT CATEQ
 GDNFRa1 227 VCSYEEREKPNCLNLQDSCKTNYICRSRLADFFTNQQPESSRSVSSCLKEN
 GDNFRa2 240 SCSYEDKEKPNCLDLRGVCR TDHLCRSRLADFHANCRASYQT VTS CPADN

DNA48613 286 -SRCLRAYLGLIGTAMTPNFVSNV-NTSVALSCTCRGSGN LQEECEMLE
 GDNFRa1 277 YADCLLAYSGLIGTVMTPNYIDSS--SLSVAPWCD CSN SGNDLEECLKFL
 GDNFRa2 290 YQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCS CRGSGNMEECEKFL

DNA48613 333 GFFSHNPCLTEAIAA-----KMRFHSQLFS
 GDNFRa1 325 NFFKDN TCLKNAIQAFNGSDVTVWQPAFPVQT TTTATTTTALRVKNKPLG
 GDNFRa2 340 R DFTENPCLR NAIQAFNGT DVNVSPKGPSFQATQA PRVEKTPSLPDDL S

DNA48613 358 Q-----DWPHP TFAVMAHQNENPAVRPQ-----
 GDNFRa1 375 PAGSENEIPTHVLP PCANLQAQK LKSNVSGNTHLCISNGNYEKEGLGASS
 GDNFRa2 390 DSTS--LGTSVIT TCTSVQE QGLKANNSKELSM CFT--ELTTNIIPGSN

DNA48613 381 ----PWVPSLF SCTLPLILLLSLW-----
 GDNFRa1 425 HITTKSMAAPP SCGLSP LLLVLVVTALSTLLSLTETS
 GDNFRa2 435 KVIK P NSGSPSRARPSAALT VLSVLM LKQAL-----

FIG. 6

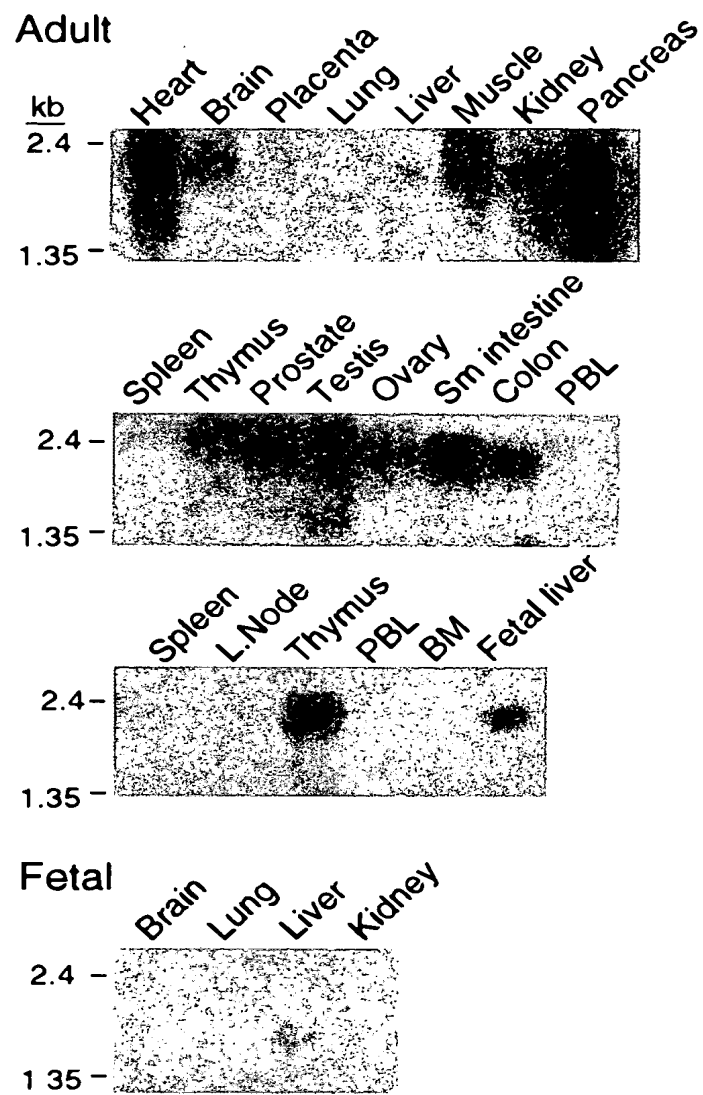


FIG. 7

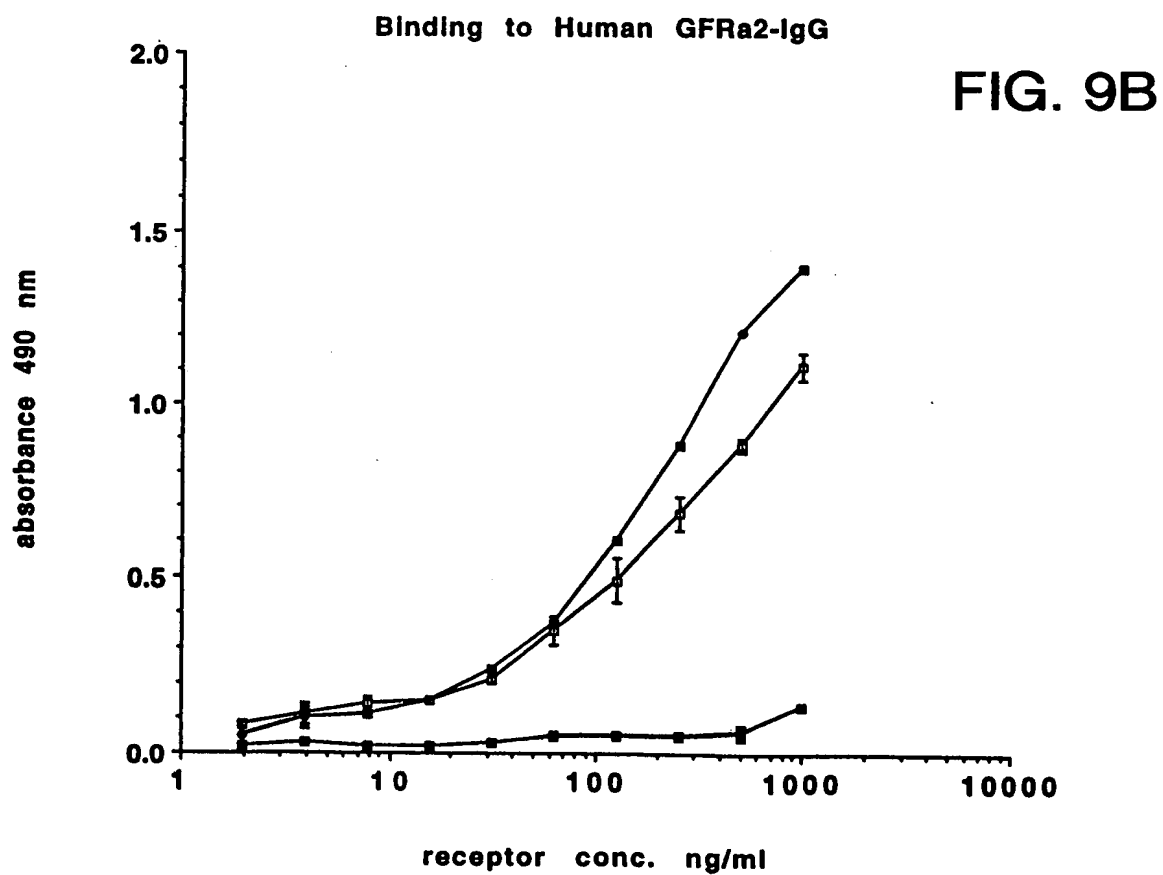
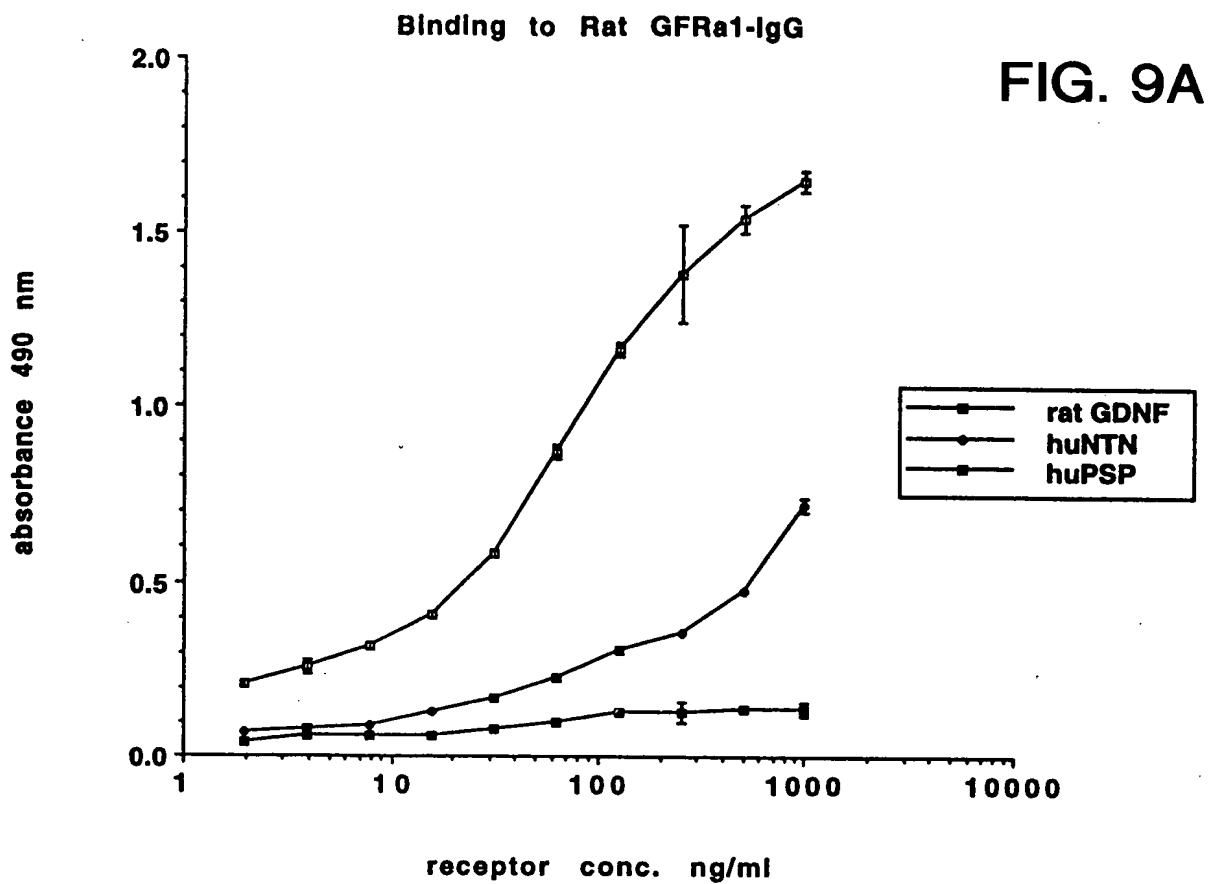
GFR α 1

GFR α 2

GFR α 3



FIG. 8



Binding to Human GFRa3-IgG

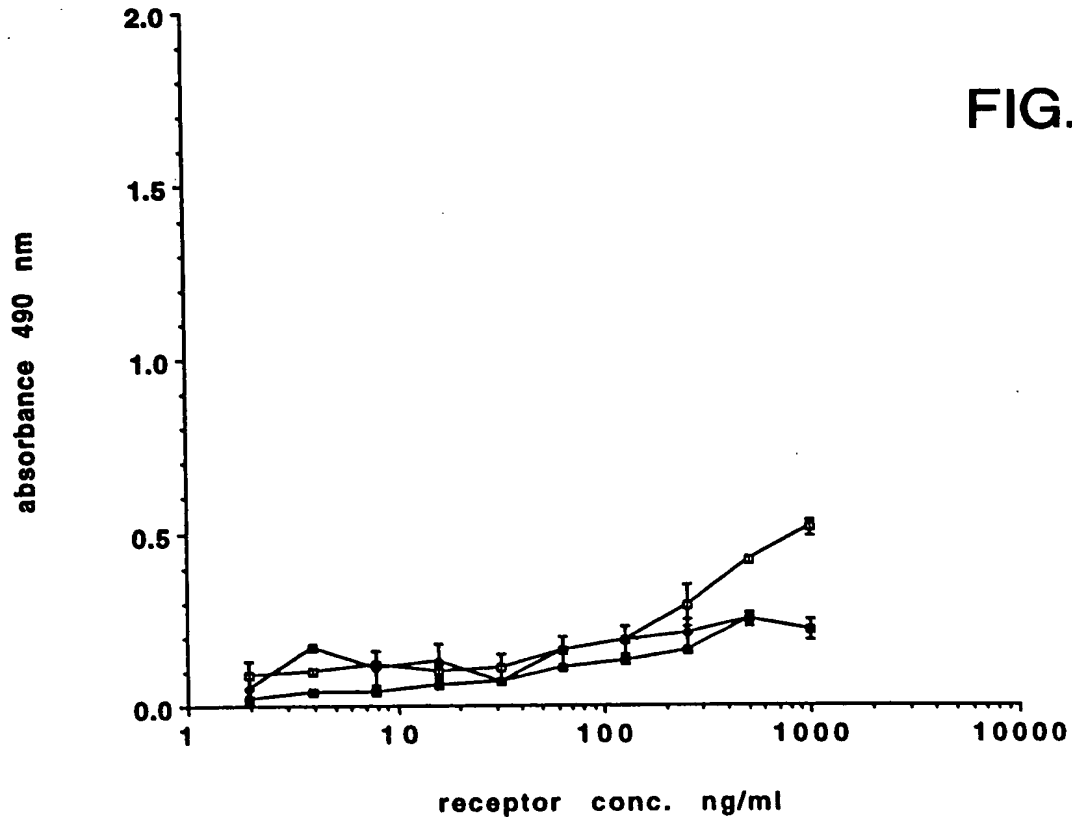


FIG. 9C

Proliferation of Ba/F3-GFRa2-mpl cells in response to NTN and GDNF

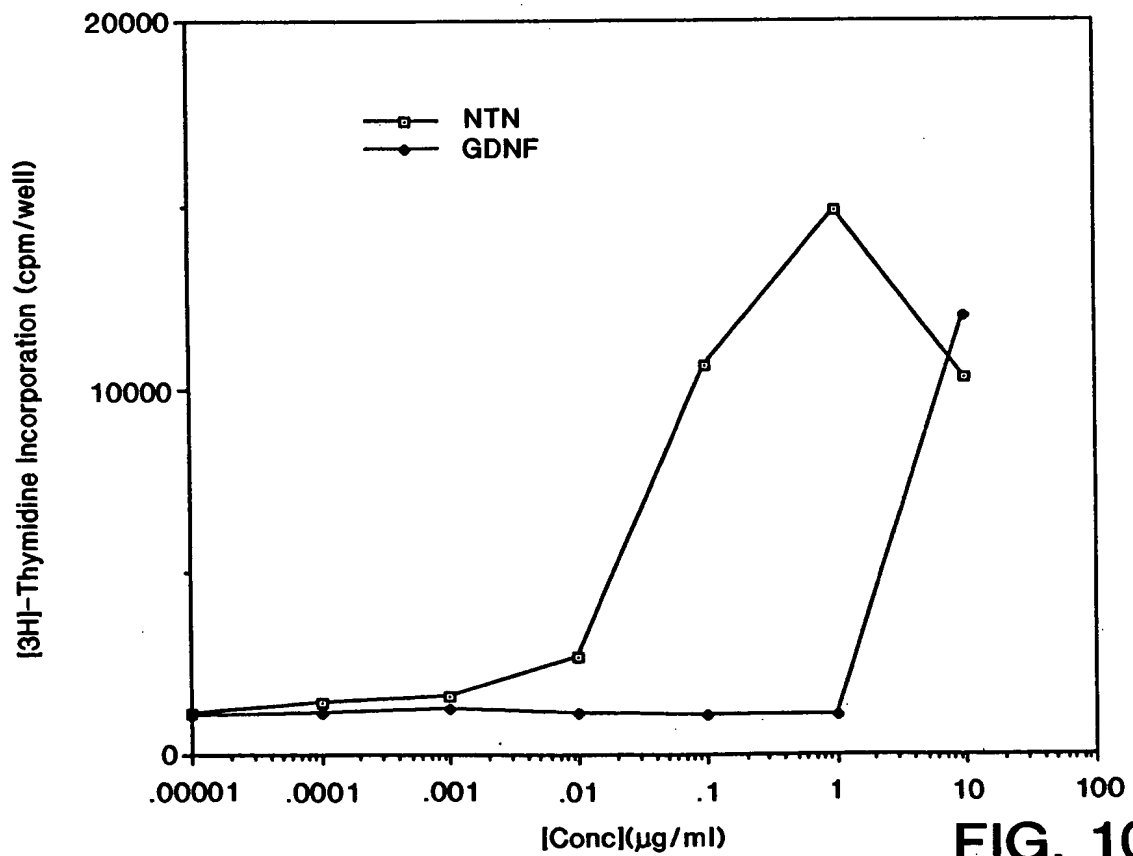


FIG. 10

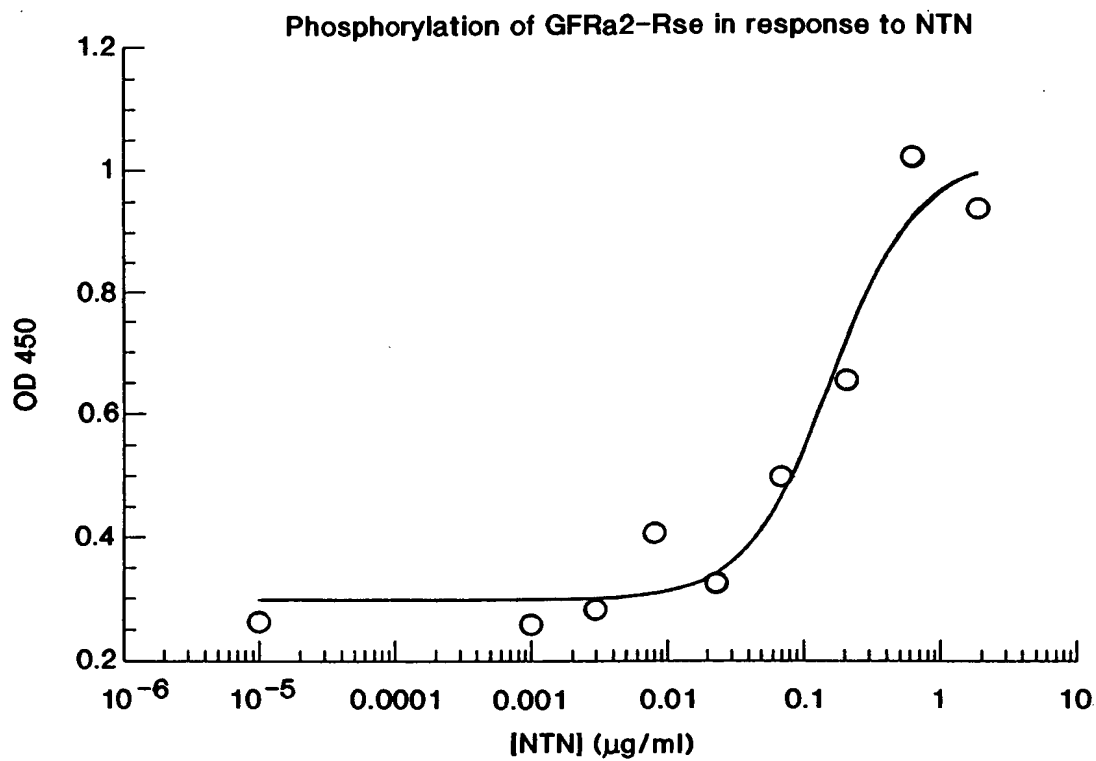


FIG. 11

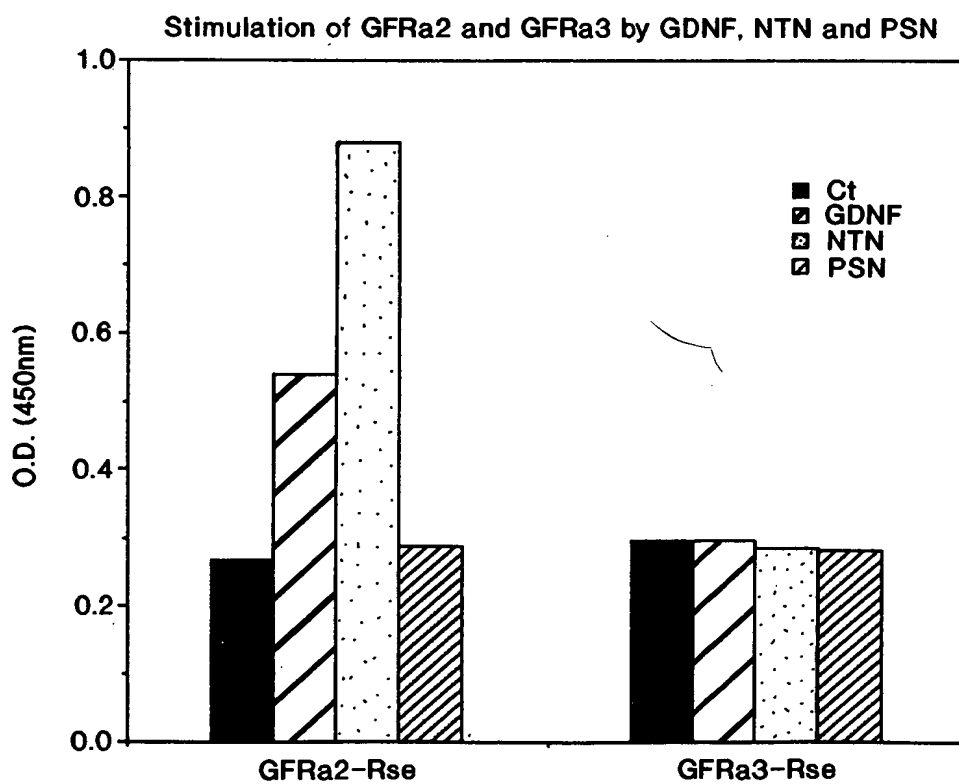


FIG. 12

Agonistic activity of anti gD mAbs in gD-alpha2-rse KIRA

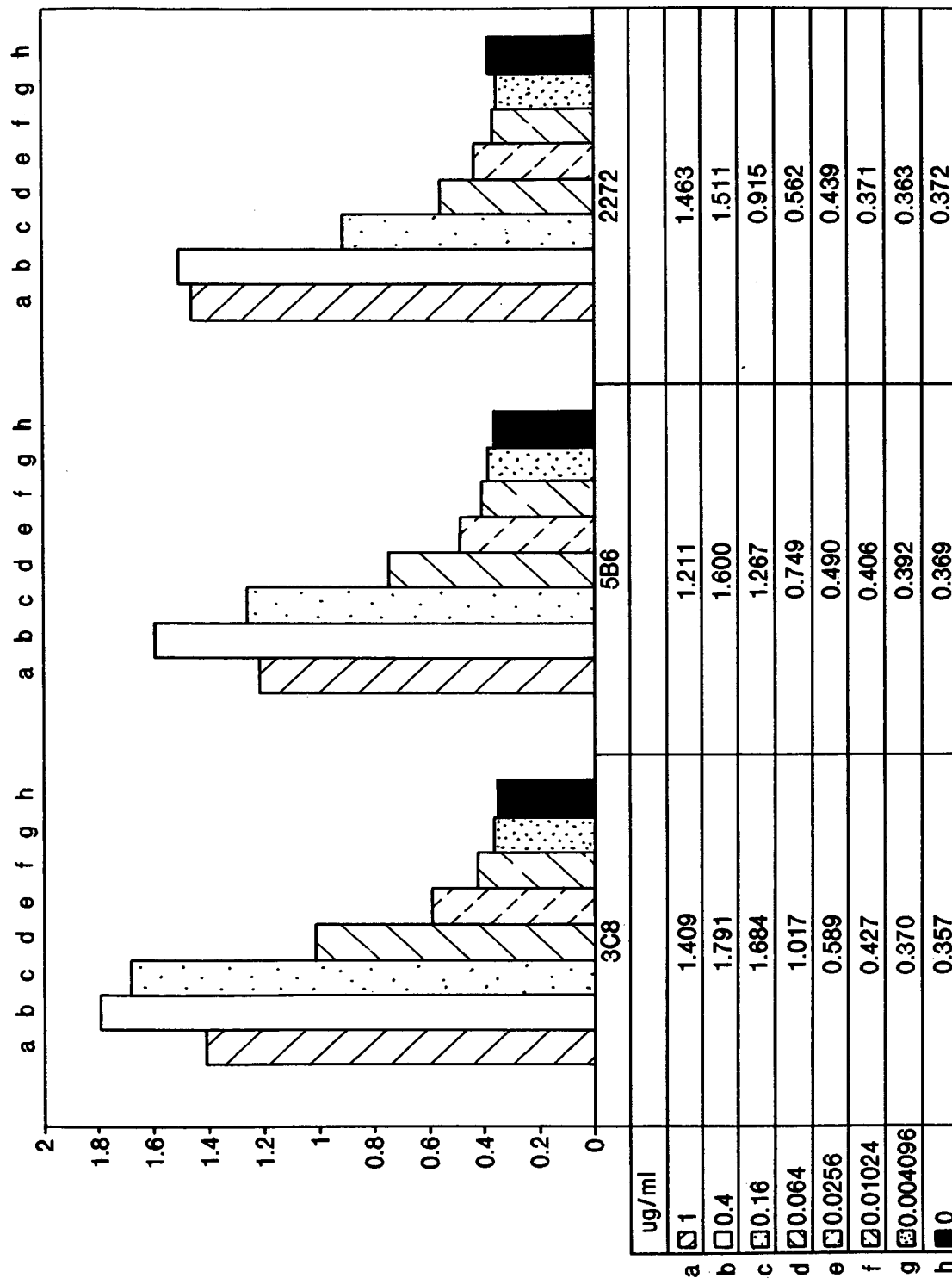


FIG. 13